In the Specification:

Please amend the specification as shown:

Please insert the following on page 1, before line 1:

Sequence Listing

The instant application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on October 1, 2010, is named 21796.txt and is 212,512 bytes in size.

Please delete the paragraph on page 9, lines 13-19 and replace it with the following paragraph:

Fig. 1: Diagram of Dendritic cell (DC)-mediated analysis of tissue samples: Dendritic cells (DCs), the most specialized antigen-presenting cells (APCs), are brought in contact with an antigen source (e.g. synovial fluid) under optimal conditions for antigen uptake and antigen processing. As a control, DCs are cultured under the same conditions in the absence of synovial fluid antigens. After maturation of DCs, antigen-loaded MHC class II molecules are purified and the respective MHC class II-associated antigenic peptides are isolated and identified. **Fig. 1 discloses SEQ ID NOS 149-152, and 151, respectively, in order of appearance.**

Please delete the paragraph on page 9, lines 29-34 replace and it with the following paragraph:

Fig. 2C: ION-TRAP MS/MS spectrum of the doubly charged peptide ion at m/z 977.1. The fragmentation masses, together with the mass of the parent ion, were searched against a non-redundant human database by using the SEQUEST algorithm. The retrieved sequence MPKNVVFVIDKSGSMSGR (one-letter-code) **(SEQ ID NO: 142)** corresponded to the dominant epitope ITIH4 (271-288) of the inter-alpha-trypsin inhibitor. The positions of the assigned series of N-terminal B-ions and C-terminal Y-ions are marked.

Please delete the paragraph on page 10, lines 1-8 and replace it with the following paragraph:

Fig. 3: Summary of the differential binding capacity of the tested candidate RA antigens in the context of binding to the *HLA-DRB1*0401* allele. The putative *HLA-DRB1*0401* binding motif is boxed in grey. and. As a measure for affinity, the peptide concentration was determined that was needed to reduce binding of a fixed amount of biotinylated HA(307-319) peptide by 50% (IC_{50}) through competition. The reciprocal (1/ IC_{50}) directly correlates with peptide affinity. As a reporter biotinylated HA(307-319) peptide from influenza hemagglutinin (Rothbard, J.B. et al., Cell 52 (1988) 515-523) was included in the study. **Fig. 3 discloses SEQ ID NOS 143, 1, 9, 15, 21, 26, 28, 35, 65, 68, and 72, respectively, in order of appearance.**

Please delete the paragraph on page 39, lines 1-3 and replace it with the following paragraph:

HA(307-319), PKYVKQNTLKLAT **(SEQ ID NO: 143)**, is an immunodominant epitope from influenza virus hemagglutinin that binds well to HLA-DR4 molecules and was used as a reporter peptide in an *in vitro* peptide binding assay (Rothbard, J.B. et al., Cell (1988) 52:515-523).

Please delete the paragraphs on page 41, line 24 to page 42, line 3 and replace them with the following paragraphs:

GILT is constitutively expressed in antigen-presenting cells, such as dendritic cells, macrophages and B cells, and facilitates unfolding of endocytosed antigens in MHC class II-containing compartments (MIIC) by enzymatically reducing disulfide bonds (Phan, U.T. et al., J Biol Chem 275 (2000) 25907-25914). Direct binding of GILT to HLA-DR molecules has been reported for B cells (Arunachalam, B. et al., J Immunol 160 (1998) 5797-5806). A rather long second epitope of GILT was found to bind to HLA-DR3 molecules: the 22-mer GILT (38-59) having the amino acid sequence SPLQALDFFGNGPPVNYKTGNL **(SEQ ID NO: 144)** (Chicz, R.M. et al., J Exp Med 178 (1993) 27-47).

In addition to GILT (192-207), another epitope of the same protein was identified in several RA samples, but also in control samples: GILT (210-227) with the amino acid sequence QPPHEYVPWVTVNGKPLE **(SEQ ID NO: 145)**. This epitope was accompanied by 3 other length variants: the 16-mer GILT (210-225), the 17-mer GILT (210-226) and the 19-mer GILT (210-228).

Please delete the paragraph on page 54, lines 14-21 and replace it with the following paragraph:

Interestingly, the analysis elucidated a second epitope of the same protein, which was highly abundant in all RA and control samples: the 16-mer SH3BGRL3 (29-44) with the amino acid sequence DGKRIQYQLVDISQDN **(SEQ ID NO: 146)**. In addition multiple length variants of the same epitope were found in most samples as well. As judged from the shortest length variant, SH3BGRL3 (31-42), the epitope contains almost similar *DRB1*0401* anchor residues compared with SH3BGRL3 (15-26): 33I serves as a P1 anchor, 36Q as a P4 anchor and 38V as a P6 anchor (binding score -2). This similarity is reflected by comparable binding scores.

Please delete Table 1 and replace it with the following Table:

Table 1: HLA-DR associated peptide antigens from serum and synovial fluid of patients with mostly non-erosive RA.

SEQ. ID. NO.	RA-type[a]	RF[b] (IU/ml)	Sample[c]	Haplo-type[d]	Length	Sequence[e]	*DRB1*0401*-binding score[f]	Protein source[g]
1	N	-	S	1	14	GDRGMQLMHANAQR	1%	Interferon-gamma-inducible lysosomal thiol reductase (192-205)
2	N	6.8	S	3	17	GDRGMQLMHANAQRTDA		
3	N	6.8	S	3	16	GDRGMQLMHANAQRTD		
2	N	9.1	Syn	4	17	GDRGMQLMHANAQRTDA		
3	N	9.1	Syn	4	16	GDRGMQLMHANAQRTD		
3	E	20.7	S	3	16	GDRGMQLMHANAQRTD		
58	N	9.1	Syn	4	17	NIQPIFAVTSRMVKTYE	2%	Integrin beta-2 (315-331)
58	N	9.1	S	4	17	NIQPIFAVTSRMVKTYE		
59	N	9.1	S	4	19	ENNIQPIFAVTSRMVKTYE		
60	N	153	S	5	17	NKVFGEDSVGVIFKNGD	3%	Phosphatidylinositol-4,5-bisphosphate 3-kinase (792-808)
60	N	88	S	5	17	NKVFGEDSVGVIFKNGD		
61	N	9.1	S	4	16	YPEQLKMTVVKLISHR	2%	Urokinase-type plasminogen activator
61	N	9.1	Syn	4	16	YPEQLKMTVVKLISHR		

								(328-343)
62	N	153	S	5	16	KNTLYLQMNSLRAEDT	1%	Immunglobulin heavy chain V-III region (V_H26) (95-110)
62	N	88	S	5	16	KNTLYLQMNSLRAEDT		
63	N	153	S	5	16	NGGHYTYSENRVEKDG	8%	DJ-1 protein (135-150)
63	N	88	S	5	16	NGGHYTYSENRVEKDG		

143	strong HLA-DRB1*0401 binder	PKYVKQNTLKLAT[h (i)]	1%	Influenza Haemagglutinin (307-319)
147	moderate HLA-DRB1*0401 binder	KHKVYACEVTHQGLS[h (ii)]	2%	Immunglobuline kappa (188-202)
148	weak HLA-DRB1*0401 binder	KTIAYDEEARR[h (iii)]	> 10%	*M. tuberculosis* Hsp65 (3-13)

[a]RA-type of the patient based on clinical diagnosis: persistant erosive (E) or persistent non-erosive (N) RA

[b]Rheumatoid factor

[c]Sample description: dendritic cells pulsed with serum (S) or synovial fluid (Syn)

[d]Haplotype of the buffy coat: (1) *HLA-DRB1*0401, *03011*; (2) *HLA-DRB1*0401, *0304*; (3) *HLA-DRB1*0401, *1301*; (4) *HLA-DRB1*0401, *0701*; (5) *HLA-DRB1*0401, *0407*

**0401, *1301*; (4) *HLA-DRB1*0401, *0701*

[e]Sequences of the RA-derived peptides in one-letter-code. The *HLA-DRB1*0401* binding motif is boxed in grey.

[f]Score of the epitope in context of the *HLA-DRB1*0401* allele based on the TEPITOPE program (Hammer, J. et al., Adv Immunol 66 (1997) 67-100).

[g]Protein name according to the Swiss-Prot / TrEMBL database. The numbers in brackets represent the shortest length variant of the respective epitope.

[h (i)] Rothbard, J.B. et al., Cell 52 (1988) 515-523. [h (ii)] Chicz, R.M. et al., J Exp Med 178 (1993) 27-47. [h (iii)] van Schooten, W.C. et al., Eur J Immunol 19 (1989) 2075-2079.